

FIG. 1A

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

GTCGACCCACGCGTCCGCACTCAACAATGCCCTGCCCTCTGACTGCACCGTCCCGCCGCGCTGCCGCGCGCGCC 79

CAAGCCAAGTCGAGCGGGGCGTTGCCACCGACGGCACAGCCCTTGGGCCCGCCCGGACCAAGGAGGTGAGCCGCGCG 158

CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCGCCAGGTGCCCGCAGCCCGCCGCGCGAG ATG CAC AGC CCG 233

P G L L A L W L C A V L C A S A R G G S 24
CCT GGG CTC CTG GCG CTG TGG TGC GCT GGT CTG TGC GCA TCG GCG CGC GGG GGC AGC 293

D P Q P G P G R P A C P A P C H C Q E D 44
GAC CCC CAG CCT GGC CCG GCG CGT CCC GCG TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC 353

G I M L S A D C S E L G L S V V P A D L 64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG 413

D P L T A Y L D L S M N L T E L Q P G 84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT 473

L F H H L R F L E L R L S G N H L S H 104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTC CCG CTC TCA GGG AAC CAC CTC TCA CAC 533

I P G Q A F S G L H S L K I L M L Q S N 124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC 593

FIG.1B

Q L R G I P A E A L W E L P S L Q S L R 144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC 653

L D A N L I S L V P E R S F E G L S L 164
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC TCC CTC 713

R H L W L D D N A L T E I P V R A L N N 184
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC 773

L P A L Q A M T L A L N H I R H I P D Y 204
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC CAT CCT GAC TAT 833

A F Q N L T S L V L H L L H N R I Q H 224
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAC CAT CTA CAT AAC AAC CGC ATC CAG CAT 893

V G T H S F E G L H N L L E T L L D L N Y N 244
GTG GGG ACC CAG AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTA GAC GAC CTG AAC TAT AAT 953

E L Q E F P L A I R T L L G R L Q E L G F 264
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC 1013

H N N I K A I P E K A F M G N P L L Q 284
CAT AAC AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC AAC CCT CTC CTG CAG 1073

T I H F Y D N P I Q F V G R S A F Q Y L 304
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG 1133

FIG. 1C

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S   K   L   H   T   L   S   L   N   G   A   T   D   I   Q   E   F   P   D   L   324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC 1193

K   G   T   T   S   L   E   I   L   T   L   T   R   A   G   I   R   L   P   344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA 1253

P   G   V   C   Q   Q   L   P   R   L   R   I   L   E   L   S   H   N   Q   I   364
CCG GGA GTG TGC CAA CAG CTG CCT AGG CTC CGA ATC CTG GAG CTG TCT CAT AAT CAG ATC 1313

E   E   L   P   S   L   H   R   C   Q   K   L   E   E   I   G   L   R   H   N   384
GAG GAG TTA CCC AGC CTG CAG CAC AGA TGT CAG AAG CTG GAG GAA ATT GGC CTC CGA CAT AAC 1373

R   I   K   E   I   G   A   D   T   F   S   Q   L   G   S   L   Q   A   L   D   404
AGG ATC AAG GAA ATT GGT GCA GAT ACC TTC AGC CAG CTG GGC TCC TTG CAA GCT TTA GAC 1433

L   S   W   N   A   I   R   A   I   H   P   E   A   F   S   T   L   R   S   L   424
CTG AGT TGG AAT GCC ATC CGT GCA GAT ACC TTC AGC CAC CCT GAG GCT TTC TCA ACC CTT CGA TCC TTG 1493

V   K   L   D   L   T   D   N   Q   L   T   T   L   P   L   A   G   L   G   G   444
GTT AAG CTG GAC CTG ACT GAC AAC CAG CTG ACC ACA CTG CCC CTG GCT GGG CTG GGA GGC 1553

L   M   H   L   K   L   K   G   N   L   A   L   S   Q   A   F   S   K   D   S   464
CTG ATG CAC CTG AAG CTC AAA GGG AAC TTG GCC CTG TCT CAG GCC TTC TTC TCC AAG GAC AGT 1613

F   P   K   L   R   I   L   E   V   P   Y   A   Y   Q   C   C   A   Y   G   I   484
TTC CCA AAA CTG AGG ATC CTG GAG GTG CCC TAC GCC TAC CAG TGC TGT GGC TAC GGC ATC 1673
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FIG.1D

C	A	S	F	F	K	T	S	G	Q	W	Q	A	E	D	F	H	P	E	E	504
TGT	GCC	AGC	TTC	TTC	AAG	ACC	TCT	GGG	CAG	TGG	CAG	GCC	GAG	GAC	TTT	CAT	CCA	GAA	GAA	1733
E	E	A	P	K	R	P	L	G	L	L	A	G	Q	A	E	N	H	Y	D	524
GAG	GAG	GCA	CCA	AAG	AGG	CCC	CTG	GGT	CTC	CTT	GCT	GGA	CAA	GCT	GAG	AAC	CAC	TAT	GAC	1793
L	D	L	D	E	L	Q	M	G	T	E	D	S	K	P	N	P	S	V	Q	544
CTA	GAC	CTG	GAT	GAG	CTC	CAG	ATG	GGG	ACA	GAG	GAC	TCA	AAG	CCA	AAC	CCC	AGT	GTC	CAG	1853
C	S	P	V	P	G	P	F	K	P	C	E	H	L	F	E	S	W	G	I	564
TGC	AGC	CCT	GTT	CCA	GGC	CCC	TTC	AAG	CCC	TGC	GAG	CAC	CTC	TTT	GAG	AGC	TGG	GGC	ATC	1913
R	L	A	V	W	A	I	V	L	L	S	V	L	C	N	G	L	V	L	L	584
CGC	CTT	GCT	GTG	TGG	GCC	ATC	GTG	CTG	CTC	TCC	GTA	CTC	TGT	AAC	GGG	CTG	GTG	CTG	CTG	1973
T	V	F	A	S	G	P	S	P	L	S	P	V	K	L	V	V	G	A	M	604
ACA	GTC	TTT	GCC	AGC	GGA	CCC	AGC	CCG	CTG	TCC	CCC	GTC	AAG	CTT	GTG	GTG	GGT	GCG	ATG	2033
A	G	A	N	A	L	T	G	I	S	C	G	L	L	A	S	V	D	A	L	624
GCA	GGC	GCC	AAC	GCC	CTG	ACG	GGC	ATT	TCC	TGT	GGT	CTC	CTG	GCC	TCT	GTG	GAC	GCC	TTG	2093
T	Y	G	Q	F	A	E	Y	G	A	R	W	E	S	G	L	G	C	Q	A	644
ACC	TAT	GGT	CAG	TTC	GCT	GAG	TAT	GGA	GCC	CGC	TGG	GAG	AGC	GGT	CTG	GGC	TGC	CAG	GCT	2153
T	G	F	L	A	V	L	G	S	E	A	S	V	L	L	L	T	L	A	A	664
ACG	GGC	TTC	CTG	GCT	GTC	CTG	GGT	TCA	GAG	GCG	TCG	GTG	CTG	CTG	CTC	ACA	CTG	GCG	GCC	2213

FIG. 1E

V	Q	C	S	I	S	V	T	C	V	R	A	Y	G	K	A	P	S	P	G	684
GTG	CAG	TGC	AGC	ATC	TCT	GTG	ACC	TGC	GTC	CGA	GCC	TAC	GGG	AAG	GCG	CCG	TCG	CCT	GGC	2273
S	V	R	A	G	A	L	G	C	L	A	L	A	G	L	A	A	A	L	P	704
AGC	GTC	CGC	GCA	GGC	GCA	CTG	GGA	TGC	CTG	GCG	CTG	GCC	GGG	CTG	GCC	GCA	GCA	CTG	CCG	2333
L	A	S	V	G	E	Y	G	A	S	P	L	C	L	P	Y	A	P	P	E	724
CTG	GCC	TCG	GTG	GGA	GAG	TAT	GGC	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCC	CCA	CCC	GAG	2393
G	R	P	A	A	L	G	F	A	V	A	L	V	M	M	N	S	L	C	F	744
GGC	CGG	CCG	GCC	GCC	CTG	GGC	TTC	GCT	GTA	GCC	CTG	GTG	ATG	ATG	AAC	TCG	CTC	TGC	TTC	2453
L	V	V	A	G	A	Y	I	K	L	Y	C	D	L	P	R	G	D	F	E	764
CTG	GTG	GTG	GCC	GGC	GCC	TAC	ATC	AAG	CTC	TAC	TGT	GAC	CTG	CCA	CGG	GGT	GAC	TTT	GAG	2513
A	V	W	D	C	A	M	V	R	H	V	A	W	L	I	F	A	D	G	L	784
GCC	GTG	TGG	GAC	TGC	GCC	ATG	GTG	CGC	CAC	GTG	GCC	TGG	CTC	ATC	TTT	GCA	GAT	GGC	CTC	2573
L	Y	C	P	V	A	F	L	S	F	A	S	M	L	G	L	F	P	V	T	804
CTC	TAC	TGC	CCC	GTG	GCC	TTC	CTC	AGC	TTT	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACC	2633
P	E	A	V	K	S	V	L	L	V	V	L	P	L	P	A	C	L	N	P	824
CCC	GAG	GCT	GTG	AAG	TCA	GTC	CTT	CTG	GTG	GTG	CTG	CCT	CTG	CCT	GCC	TGC	CTC	AAC	CCA	2693
L	L	Y	L	L	F	N	P	H	F	R	D	D	L	R	R	L	W	P	S	844
CTG	CTC	TAC	CTG	CTC	TTC	AAC	CCT	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTC	TGG	CCA	AGC	2753

FIG. 1F

P R S P G P L A Y A A G E L E K S S C 864
CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC 2813

D S T Q A L V A F S D V D L I L E A S E 884
GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG 2873

A G Q P P G L E T Y G F P S V T L I S R 904
GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA 2933

H Q P G A T R L E E G N H F I E S D G T K 924
CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG 2993

F G N P P Q P P M K G E L L K A E G A T 944
TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG AAG GCA GAG GGA GCC ACT 3053

L A G C G S S V G G A L W P S G S L F A 964
TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC 3113

S H L * 968
TCT CAC TTG TAA 3125

ATATCCCTCTGTGTTGTCCCTCTCCCCATCCAATGATGGCTGCTTATAAAGAAAGACAACCTCCAATAGCAAGA 3204

TGGCCAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTGTCTTGG 3283

CCTTCAGCTTCACTTTCACCCCTGGGCCTTCTCTGTCCAATCCAATACTTCTGACAGAGGCCCTGGGAAATTGCATAGGA 3362

FIG.1G

GAAAGGAGAAAGCAAAAGACAGTGAAAGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCCAGAGTGATGGGGAG 3441

GTCTCACAGAGCATGACACTGGAAGACAACCTACCAAGACATTTGGAGAGTCTCCCTGTGACATATAGAAATATAAAATG 3520

TGTTCTGCGTTCCATTAAATCTTGACCTATGCTGNGCCAAAGTGCTTCCCTGTTAAATAACACTTTGGAAGACATTGAAAA 3599

AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637

??

FIG. 2A

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
+LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f++L+
ftmzb048h1
67 LTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
+L+ L L+ N+L+++p++al+ Lp+L++L L+ N ++ +p++++f++L+
ftmzb048h1
115 SLKILMQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
+L++L+L++N Lt++p al+nLp L+ L N+++++p+++fqnL+
ftmzb048h1
163 SLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnL k<-
+L +L+L nN+++++ ++++++L+nLe+LdL++N+L+++p + + L+
ftmzb048h1
211 SLVHLHNNRIQHVGTSHSFEGLHNLETLDLNYNELQEFPL-AIRTLG 257

FIG.2B

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
+L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
ftmzb048h1
258 RLQELGFHNNIKAIEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
->nLeeLdLsnNk.LtslppgalsnLpnLeeLdLsnNnLtslppgIfqn Lk<-
+L++L+L++ ++++++p+ l++ ++Le L L + ++ lppg++q L+
ftmzb048h1
306 KLHTLSLNGATdIQEFPD--LKGTTSLEILTLTRAGIRLLPPGVCCQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
+L+ L+Ls+N+++++lp+ l+ +++Lee+ L +N+++++ ++f+ L+
ftmzb048h1
353 RLRILELSHNQIEELPS--LHRCQKLEEIGLRHNRIKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnLk<-
+L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L
ftmzb048h1
399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTTLPLAGLGGLM 446

FIG. 3A-1

Protein (species)*	Function-ligand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich α 2-GP (human)	?-?	Serum
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF- β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF- β	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP Ib	PM (EC)
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC
IpaH7.8 (Shigella flexner)	?-?	?
IpaH4.5 (Shigella flexner)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length	Consensus sequence	PIR entry
15	28 (A)	.LE.L.L..C-.LT...C...L..aL....	A31857
	29 (B)	.L.EL.L..N-.LGD.Ga..L...L..P..	
8	24	.L..L.L..N-.L...-L...LL....--.	NBHUA2
8	29	.L..L.L..N-.a.....a..a.....	BVBYN1
4	24	.L..L.a..N-.a.....L--.	S03616
8	24	.L..L.L..N-.I..-a.....a....--.	A40757
10	24	.L..L.L..N-.I..-V.....a....--.	NBHUC8
11	24	.L..L.L..N-.a..-a.....a....--.	S05390
12	24	.L..L.L..N-.L..-.....a....--.	A41748
6	24	.L..a.L..N-.I..-.....a....--.	A41781
6	24	.L..a.L..N-.a..-.....F....--.	A35272
7	24	.L..L.L..N-.L..-LP.GL...L--.	NBHUIA
14	24	.L..L.L..N-.L..-LP...LF..L--.	-
12	20	.L..L.a..N-.L..-LP-...-L--PP	A33950
6	20	.L..L.V..N-.L..-LP-...-L--P.	A35149
8	20	.L..L.a..N-.L..-LP-...-L--P.	S18248
19	24	.L..L.L..N-.L..-.....F....--.	A29943
19	24	.L..L.L..N-.I..-.....F..L--.	A36665
7	24	.L..LNL..N-.I..-a....aF..L--.	S28464
30	24	.L..L.L..N-.a..-a.....F..a--.	A29944
16	23	.L..L.LS.N-.L..-aP..a..-L--.	-
8	24	.L..L.LSNN-.a..-a.....L--.	A34210

FIG. 3B-1

Protein (species)*	Function-ligand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase--?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylate cyclase (Saccharomyces cerevisiae)	Signal transduction-RAS	PM
T-LR (Tyrpanosoma brucei)	?--?	(cytoplasm)
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	?
RAD7 (Saccharomyces cerevisiae)	DNA repair--?	Nucleus
DRT100 (Arabidopsis thaliana)	Recombination--?	?
GRR1 (Saccharomyces cerevisiae)	Signal transduction--?	Chloroplast
CCR4 (Saccharomyces cerevisiae)	Transcription--?	Cytoplasm
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	?
p34 ribosome-binding protein(rat)	RM membranes-ribosome	Nucleus
Carboxypeptidase N (human)	Stabilization-catalytic subunit	RM membrane
Intermalin (Listeria monocytogenes)	Invasion--?	(cytoplasm)
InIB (Listeria monocytogenes)	?--?	Plasma
LRR superfamily		Cell wall
		?

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L..L..N-.....	TDHUM4
2	23	.L..L..LS.N-.L.....	TVHUTT
3	23	.L..L..aT.N-.LTS.....	S06943
3	23	.LR.aNLSQN-.L...S-.....	A40026
11	23	.L..a..L..N-...G.aP-..a.SL--.	JQ1674
5	25	.L..L..a..T-.a.....F.....	A41343
7	25	.L..L..aS.T-.....LP...a..a--.	A34548
6	25	.a..L..a..NN...a.S-a.....	A40077
20	23	.L..L..L..N-.a...-a...L--.	OYBY
18	23	.L..L..LSGC..a...-a...L--.	A36359
3	23	.a..LaDI..N--LP..a.....N----	DDBYD1
5	26	.L..L..a..C..a.....a...--P	A25226
5	24	.L..LNL..N-.L.G.IP.S-a.S.--.	A46260
9	26	.L..a..L..C.NaTD..a...-L..L--.	A41529
4	23	.L..L..a..N-.LT.-LP.E-a...--.	S31286
11	22	.L..L..a..N-.I...-a--ENa..L--.	A38439
4	24	.L..LDL..N-.L...-LP...F..L--.	-
12	24	.L..L..L..N-.L...-LP..aF..L--.	A34901
13	22	NL..L..L..n-QISDI.P---L..L--T	A39930
6	22	.L..L..L..N-.L.DI...--L..L--.	C39930
	5 10 15 20 25	.L..L..L..N*.a...*a***a***a***.	

FIG. 4

>human DNA seq.

TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA
TTCCCGGGTTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTCCAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGGCCACTGGCTTCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCC
AGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCGCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACCTGTACTGTGA
CCTGCCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCCGAGGCCGTCAAGT
CTGTCCTGCTGGTGGTGCTGCCCCCTGCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGGCTTCGGCCCCCGCGC
AGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGGCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGGTGGCGGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAAAGGGCGGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT

FIG. 5

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQQGLSLPAHPASLAALAASNTTASGKLE
DTFSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGMLHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLTLAAVQCSVSVS
CVRAYGKSPSLGSRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMNSFCFLWAGAYIKLYCDLPRGDFEAWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVPLPACLNPLLYLLFNPHFRDDLRL
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

FIG. 6

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11
*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppgIfqnL
+L+LdLsN ++s++p+a+s+L++L +LdL +N+Lt+lp + +L
fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

k<*

fahr 111 M 111

FIG. 7A

ftmzb048h10	1	80	MHSPPGLLALWLCASARGSDPPQPGRPACAPCHCQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSMNNLTE
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~
ftmzb048h10	81	160	LQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLSKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEG
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~
ftmzb048h10	161	240	LSSLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLNLETLD
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~
ftmzb048h10	241	320	LNYNELQEFPLAIRTLGRLQELGEHNNNIKAIPKAFMGNPLLQTIHFYDNPIQFVGRSAFYLSKLHTLSLNGATDIOE
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~
ftmzb048h10	321	400	FPDLKGTTSEILTLTRAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEELGLRHNRIKEIGADTFSQLGSL
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~
ftmzb048h10	401	480	QALDLSWNAIRAIHPEAFSTLRSVLKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~
ftmzb048h10	481	560	AYGICASFFKTSQWQAEDEHFPEEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSVPVPGPFKPCHEHLFE
Aa_of_aambb001d112			~~~~~
fahr_human			~~~~~

FIG.8A

G	L	H	N	L	E	T	L	D	L	N	Y	N	K	L	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	AAC	ATC	AAG	GCC	120
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GGA	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCC	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GGA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540

FIG.8B

```
S      I      H      P      E      A      F      S      T      L      H      S      L      V      K      L      D      L      T      D      200
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG CTG GTC AAG CTG GAC CTG ACA GAC GAC 600

N      Q      L      T      T      L      P      L      A      G      L      G      G      L      M      H      L      K      L      K      220
AAC CAG CTG ACC ACA CTG CCC CTG GCT GGA CTT GGG GGC TTG ATG CAT CTG AAG CTC AAA 660

G      N      L      A      L      S      Q      A      F      S      K      D      S      F      P      K      L      R      I      L      240
GGG AAC CTT GCT CTC TCC CAG GCC TTC TCC AAG GAC AGT TTC CCA AAA CTG AGG ATC CTG 720

E      V      P      Y      A      Y      Q      C      C      P      Y      G      M      C      A      S      F      F      K      A      260
GAG GTG CCT TAT GCC TAC CAG TGC TGT CCC TAT GGG ATG TGT GCC AGC TTC TTC AAG GCC 780

S      G      Q      W      E      A      E      D      L      H      L      D      D      E      E      S      S      K      R      P      280
TCT GGG CAG TGG GAG GCT GAA GAC CTT CAC CTT GAT GAT GAG GAG TCT TCA AAA AGG CCC 840

L      G      L      L      A      R      Q      A      E      N      H      Y      D      Q      D      L      D      E      L      Q      300
CTG GGC CTC CTT GCC AGA CAA GCA GAG AAC CAC TAT GAC CAG CAG CTG GAT GAG CTC CAG 900

L      E      M      E      D      S      K      P      H      P      S      V      Q      C      S      P      T      P      G      P      320
CTG GAG ATG GAG GAC TCA AAG CCA CAC CCC AGT GTC CAG TGT AGC CCT ACT CCA GGC CCC 960

F      K      P      C      E      Y      L      F      E      S      W      G      I      R      L      A      V      W      A      I      340
TTC AAG CCC TGT GAG TAC CTC TTT GAA AGC TGG GGC ATC CGC CTG GCC GTG TGG GCC ATC 1020

V      L      L      S      V      L      C      N      G      L      V      L      L      L      T      V      F      A      G      G      P      360
GTG TTG CTC TCC GTG CTC TGC AAT GGA CTG GTG CTG CTG ACC GTG TTC GCT GGC GGC CCT 1080
```

FIG. 8C

```
A  P  L  P  P  V  K  F  V  V  G  A  I  A  G  A  N  T  L  T      380
GCC CCC CTG CCC CCG GTC AAG TTT GTG GTA GGT GCG ATT GCA GGC GCC AAC ACC TTG ACT 1140

G  I  S  C  G  L  L  A  S  V  D  A  L  T  F  G  Q  F  S  E      400
GGC ATT TCC TGT GGC CTT CTA GCC TCA GTC GAT GCC CTG ACC TTT GGT CAG TTC TCT GAG 1200

Y  G  A  R  W  E  T  G  L  G  C  R  A  T  G  F  L  A  V  L      420
TAC GGA GCC CGC TGG GAG ACG GGG CTA GGC TGC CGG GCC ACT GGC TTC CTG GCA GTA CTT 1260

G  S  E  A  S  V  L  L  L  L  T  L  A  A  V  Q  C  S  V  S  V      440
GGG TCG GAG GCA TCG GTG CTG CTG CTG ACT CTG GCC GCA GTG CAG TGC AGC GTC TCC GTC 1320

S  C  V  R  A  Y  G  K  S  P  S  L  A  A  V  Q  R  A  G  V  L      460
TCC TGT GTC CGG GCC TAT GGG AAG TCC CCC TCC CTG GGC AGC GTT CGA GCA GGC GTC CTA 1380

G  C  L  A  L  A  G  L  A  A  A  A  L  P  L  A  S  V  G  E  Y      480
GGC TGC CTG GCA CTG GCA GGG CTG GCC GCA CTG CCC CTG GCC TCA GTG GGA GAA TAC 1440

G  A  S  P  L  C  L  P  Y  A  P  P  E  G  Q  P  A  A  L  G      500
GGG GCC TCC CCA CTC TGC CTG CCC TAC GCG CCA CCT GAG GGT CAG CCA GCA GCC CTG GGC 1500

F  T  V  A  L  V  M  N  S  F  C  F  L  V  V  A  G  A  Y      520
TTC ACC GTG GCC CTG GTG ATG ATG AAC TCC TTC TGT TTC CTG GTC GTG GCC GGT GCC TAC 1560

I  K  L  Y  C  D  L  P  R  G  D  F  E  A  V  W  D  C  A  M      540
ATC AAA CTG TAC TGT GAC CTG CCG CGG GGC GAC TTT GAG GCC GTG TGG GAC TGC GCC ATG 1620
```

FIG. 8D

V	R	H	V	A	W	L	I	F	A	D	G	L	Y	C	P	V	A	F	560	
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680	
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
CTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC	CCC	AGG	2040
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160

FIG. 9

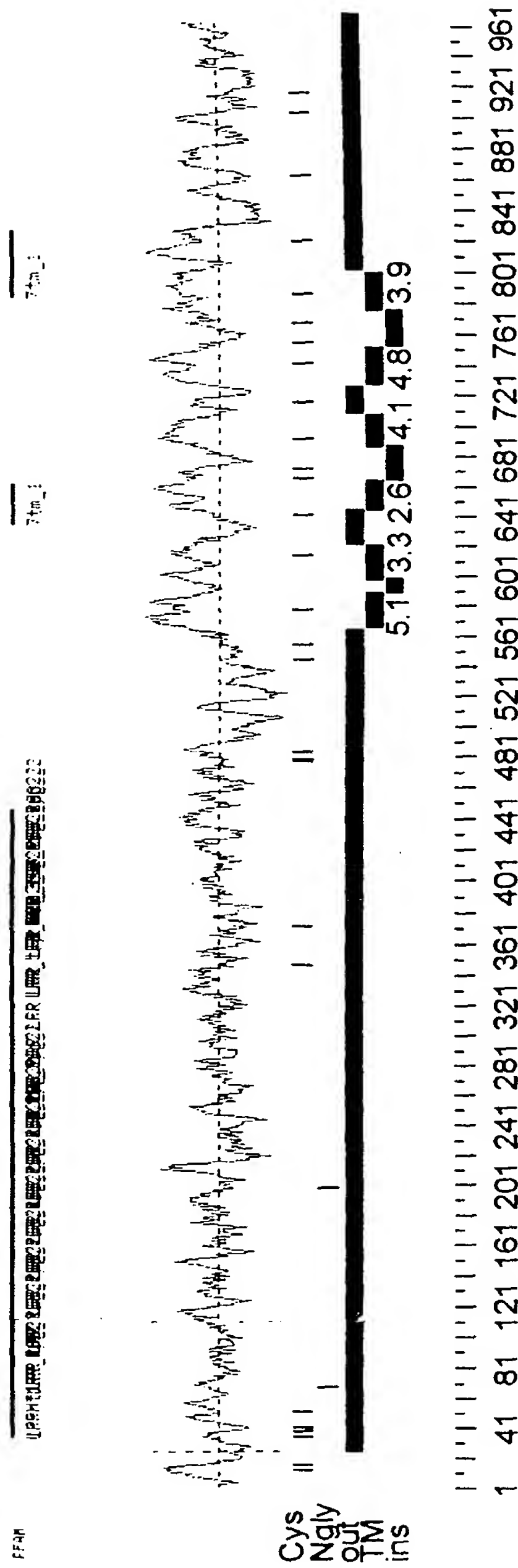


FIG. 10A

Searching for complete domains in PFAM

hmmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam

Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
<u>LRR</u>	Leucine Rich Repeat	241.4	1.3e-68	16
<u>LRRNT</u>	Leucine rich repeat N-terminal domain	27.2	0.00038	1
<u>7tm_1</u>	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
LRRNT	1/1	34	65 ..	1	31 []	27.2	0.00038
LRR	1/16	67	90 ..	1	23 []	12.4	11
LRR	2/16	91	114 ..	1	23 []	24.2	0.0031
LRR	3/16	115	138 ..	1	23 []	19.9	0.062
LRR	4/16	139	162 ..	1	23 []	16.4	0.7
LRR	5/16	163	186 ..	1	23 []	27.5	0.00031
LRR	6/16	187	210 ..	1	23 []	12.1	13
LRR	7/16	211	234 ..	1	23 []	21.6	0.019
LRR	8/16	235	257 ..	1	23 []	18.2	0.2
LRR	9/16	258	281 ..	1	23 []	19.0	0.11
LRR	10/16	282	305 ..	1	23 []	10.2	32
LRR	11/16	306	328 ..	1	23 []	5.6	1.5e+02
LRR	12/16	329	352 ..	1	23 []	8.8	52
LRR	13/16	353	374 ..	1	23 []	19.2	0.097
LRR	14/16	375	398 ..	1	23 []	16.9	0.49
LRR	15/16	399	422 ..	1	23 []	23.7	0.0042
LRR	16/16	423	446 ..	1	23 []	16.4	0.66
7tm_1	1/2	635	662 ..	51	79 ..	3.4	2.2
7tm_1	2/2	784	827 ..	207	259 .]	1.1	11

FIG. 10B

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

->aCpreCtCsp..fglvVdCsgrgLtleVPrdlP<-

aCp++C+C +++ l+ dCs++gL +vP dl

15088 34 ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD 65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

->nLeeLdLsnN.LtslppglfsnLp<-

+LdLs N+Lt+l pglf++L+

15088 67 LTAYLDLSMNnLTELQPGLFHHLR 90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

->nLeeLdLsnN.LtslppglfsnLp<-

LeeL+Ls+N+L+++p +fs+L

15088 91 FLEELRLSGNnLSHIPGQAFSGLY 114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ L L+nN+L ++p +++ Lp

15088 115 SLKILMLQNNqLGGIPAEALWELP 138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L+ N ++ +p+ +f++L+

15088 139 SLQSLRLDANIISLVPERSFEGLS 162

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L++N Lt++p +++nLp

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13

->nLeeLdLsnN.LtslppglfsnLp<-

L+ L N+++++p+ +f+nL+

15088 187 ALQAMTLALNriSHIPDYAFQNLT 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019

->nLeeLdLsnN.LtslppglfsnLp<-

+L +L+L+nN+++++l ++f++L

15088 211 SLVVLHLHNNriQHLGTHSFEGH 234

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2

->nLeeLdLsnN.LtslppglfsnLp<-

nLe+LdL++N+L+++p +++ L

15088 235 NLETLDLNYNkLQEFPV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11

->nLeeLdLsnN.LtslppglfsnLp<-

+L+eL ++nN+++ +p+++f + p

15088 258 RLQELGFHNNnIKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32

->nLeeLdLsnN.LtslppglfsnLp<-

L+ +++ +N+++ + ++f+ Lp

15088 282 LLQTIHFYDNpIQFVGRSAFQYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L++ +++++p+ +++ +

15088 306 KLHTLSLNGAmdIQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52

->nLeeLdLsnN.LtslppglfsnLp<-

+Le L L + +++ lp+g +++Lp

15088 329 SLEILTLTRAgIRLLPSGMCQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L Ls+N++++lp+ ++ ++

15088 353 RLRVLELSHnqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49

->nLeeLdLsnN.LtslppglfsnLp<-

+Lee+ L++N++ ++ ++fs+L+

15088 375 KLEEIGLQHNrIWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ LdLs N ++s++p++fs L

15088 399 SLQALDLSWNaIRSIHPEAFSTLH 422

FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

->nLeeLdLsnN.LtSlppglfsnLp<-

+L +LdL +N+Lt+lp ++L

15088 423 SLVKLDLTDNqLTTLPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

->dWpfGsalCklvtaldvvnmyaSillLta<-

+W G ++C+ +++l v+ + aS+llLt+

15088 635 RWETG-LGCRATGFLAVLGSEASVLLLTl 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

*->ICWlPyfivllldtlc.lsiimsstCelervlptallvtlwLayvNs

l+ P +++ +l ++ +++++++v l++ ++

15088 784 LLYCPVAFLSFASMLGIFPV-----

TPEAVKSVLLVVLPLPA 820

cINPiIY<-*

cINP++Y

15088 821 CLNPLLY 827

FIG. 11A

Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - -
HMM file: /ddm/robison/smart/smart.all.hmms
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq
- - - - -
Query: 15088
- - - - -
Scores for sequence family classification (score includes all domains):
Model Description Score E-value N

LRR_typ_2 247.2 2.3e-70 14
LRR_PS_2 78.1 1.8e-19 13
LRR_sd22_2 33.5 4.9e-06 5
lrrnt1 25.7 0.0011 1
LRR_bac_2 11.8 3 7
LRR_RI_2 5.4 7.7 4

Parsed for domains:
Model Domain seq-f seq-t hmm-f hmm-t score E-value

lrrnt1 1/1 34 70 .. 1 38 [] 25.7 0.0011
LRR_PS_2 1/13 64 87 .. 1 24 [] 1.9 1.2e+02
LRR_typ_2 1/14 64 88 .. 1 24 [] 12.6 2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	20	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	209	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	10.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

LRR_typ_2	10/14	327	350 ..	1	24 []	3.1	29
LRR_bac_2	6/7	351	370 ..	1	20 []	14.6	1.3
LRR_PS_2	10/13	351	372 ..	1	24 []	10.8	8
LRR_sd22_2	3/5	351	372 ..	1	22 []	7.6	16
LRR_typ_2	11/14	351	373 ..	1	24 []	18.8	0.13
LRR_RI_2	4/4	351	378 ..	1	28 []	2.6	19
LRR_PS_2	11/13	373	396 ..	1	24 []	2.3	1e+02
LRR_typ_2	12/14	374	396 ..	1	24 []	6.8	10
LRR_sd22_2	4/5	397	418 ..	1	22 []	7.0	19
LRR_PS_2	12/13	397	419 ..	1	24 []	13.6	3.4
LRR_typ_2	13/14	397	420 ..	1	24 []	30.4	4.3e-05
LRR_bac_2	7/7	421	440 ..	1	20 []	5.8	18
LRR_sd22_2	5/5	421	441 ..	1	22 []	3.7	49
LRR_PS_2	13/13	421	442 ..	1	24 []	5.5	39
LRR_typ_2	14/14	421	444 ..	1	24 []	21.6	0.018

Alignments of top-scoring domains:

lrrntl: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011

-->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<--
+CPapC+C ++ ++ dCs++gL +vP dl + t +

15088 34 ACPAPCHCQEdGIMLSADCSSELGLS--AVPGDLPLTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02

-->LtsL.qvLdLsnNnLsGeIPsslgn<--

L L+ +LdLs NnL+ e+ + l+

15088 64 LDPLtAYLDLSMNNLT-ELQPGLFH 87

FIG. 11D

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
->LpnL.reLdsNqLtsLppgaFqg<-
L L+ LdLs N+Lt+L pg+F++
15088 64 LDPLtAYLDLSMNNLTQLPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
->PpsLkeLnvsnNrLteLPeL<-
+L+eL+ s+N+L+ P
15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
->LtsLqvLdsNnNsGeIPsslgn<-
L+ L++L+Ls+N+Ls +IP + ++
15088 89 LRFLEELRLSGNHLs-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
->LpnLreLdsNqLtsLppgaFqg<-
L+ L+eL+Ls+N+L+++P +aF+g
15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
->npsLreLdsNk1.gdeGaraLaealks<-
++ L+eL+Ls+N+L+++ G + ++L s
15088 89 LRFLEELRLSGNHLSHIPG--QAFSGLYS 115

FIG. 11E

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
-->PpsLkeLnvsnNrLteLPeL<--
 sLk+L +nN+L P+
15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
-->LtsLqvLdLsnNnLsGeIPsslgn<--
 L sL++L L+nN+L G + l+
15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
-->LpnLreLdLsnNqLtsLPpgaFqg<--
 L +L+ L L+nNqL +P++a++
15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
-->PpsLkeLnvsnNrLteLPeL<--
 psL++L+ + N ++ Pe
15088 137 LPsLQSLRLDANLISLVPER 156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
-->LtsLqvLdLsnNnLsGeIPsslgn<--
 L+sLq+L+L N +s +P+ +
15088 137 LPsLQSLRLDANLIS-LVPERSFE 159

FIG. 11F

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
->LpnLrelDlsnNqLtsLPpgaFqg<-
Lp+L++L+L+ N ++ +P++ F+g
15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
->LtsLqvLdsnNnLsGeIPsslgn<-
L+sL++L L +N L+ eIP n
15088 161 LSSLRHLWDDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
->LpnLrelDlsnNqLtsLPpgaFqg<-
L++Lr+L L++N+Lt++P +a+++
15088 161 LSSLRHLWDDNALTEIPVRALNN 184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
->LtnLeeLdLsqNkI.....kklENLde<-
L+ L++L+L +N +++ + + + NL
15088 161 LSSLRHLWDDNALTEIPVRALNNLPA 187

LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
->npsLrelDlsnNklgdeGaral..aealks<-
++sLr L+L +N l++ +raL++ aL++
15088 161 LSSLRHLWDDNALTEIPVRALnnLPALQA 190

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
-->LtsLqvLdLsnNnLsGeIPsslgn<--
L+ Lq L+ N++s +IP+ ++
15088 185 LPALQAMTLALNRIS-HIPDYAFQ 207

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
-->LpnLrelDlsnNqLtsLPpgaFqg<--
Lp+L+ L N+++++P+ aFq+
15088 185 LPALQAMTLALNRISHIPDYAFQN 208

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
-->LtsLqvLdLsnNnLsGeIPsslgn<--
LtsL+vL+L+nN++ s+
15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
-->LpnLrelDlsnNqLtsLPpgaFqg<--
L++L +L+L+nN+++++L F+g
15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
-->npsLrelDlsnNklgdeGaraLaealks<--
++sL +L+L nN + G + e+L+
15088 209 LTSLVVLHLHNNRIQHLGTHSF-EGLHN 235

FIG. 11H

LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
->LtnLeeLdlsqNkI.....kkiENLde<-
Lt L++L L +N+I++ +++++E+L++
15088 209 LTSLVVLHLHNNRRIqhlgtHSFEGLHN 235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
->PpsLkeLnvsnNrLteLPeL<-
++L++L+ ++N+L e+P
15088 233 LHNLETLDLNYNKLQEFPPVA 252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
->LpnLreLdsnNgLtsLppgaFqg<-
L+nL++LdL++N+L++ P + +
15088 233 LHNLETLDLNYNKLQEFPPVAI-RT 255

LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
->LtsLqvLdsnNnLsGeIPsslgn<-
L++L++LdL++N+L e+P +
15088 233 LHNLETLDLNYNKLQ-EFPVAIRT 255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
->PpsLkeLnvsnNrLteLPeL<-
+L+eL+ nN+++ Pe
15088 256 LGRLQELGFHNNNNIKAIPEK 275

FIG. 11I

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
->LtsLqvLdLsnNnLsGeIPsslgn<-
L +Lq+L ++nNn+ IP+ +
15088 256 LGRLQELGFHNNNIK-AIPEKAFM 278

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
->LpnLreLdLsnNqLtsLppgaFqg<-
L+ L+eL +nN++++P+ aF g
15088 256 LGRLQELGFHNNNIKAIPEKAFMG 279

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
->LpnLreLdLsnNqLtsLppgaFqg<-
++L+ L L + ++ LP+g++q
15088 327 TTSLIILTLTRAGIRLLPSGMCQQ 350

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
->PpsLkelNvsnNrLteLPeL<-
p+L+ L s+N+++eLP L
15088 351 LPRLRVLELSHNQIEELPSL 370

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
->LtsLqvLdLsnNnLsGeIPsslgn<-
L++L+vL+Ls+N++ e+Ps l +
15088 351 LPRLRVLELSHNQIE-ELPS-LHR 372

FIG. 11J

LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
-->LtnLeeLdLsqNkIkkIENLde<--
L +L++L+Ls+N+I+ + L+
15088 351 LPRLRVLELSHNQIEELPSLHR 372

LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
-->LpnLreLdLsnNqLtsLPpgaFqg<--
Lp Lr+L Ls+Nq++LP + ++
15088 351 LPRLRVLELSHNQIEELP-SLHRC 373

LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
-->npsLreLdLsnNklgdeGaraLaealks<--
+p+Lr+L Ls+N + + ++ L++
15088 351 LPRLRVLELSHNQIEELPSLHRCQKLEE 378

LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
-->LtsLqvLdLsnNnLsGeIPsslgn<--
+++L+++ L++N++ ++++
15088 373 CQKLEEEIGLQHNRIWEIGADTFsq 396

LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
-->LpnLreLdLsnNqLtsLPpgaFqg<--
+L+e L++N++ ++ +++F+
15088 374 -QKLEEEIGLQHNRIWEIGADTFsq 396

FIG. 11K

LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
->LtnLeeLdLsqNkIkkiENLde<-
L+ L+ LdLs+N I++i
15088 397 LSSLQALDLSWNAIRSIHPEAF 418

LRR_ps_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
->LtsLqvLdLsnNnLsGeIPsslgn<-
L+sLq LdLs+N + +I ++ ++
15088 397 LSSLQALDLSWNAIR-SIHPEAFS 419

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
->LpnLreLdLsnNqLtsLppgaFqg<-
L++L+ LdLs+N+++s++p+aF+
15088 397 LSSLQALDLSWNAIRSIHPEAFST 420

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
->PpsLkeLnvsnNrLteLPeL<-
+sL +L+ +N+Lt+LP
15088 421 LHSLVKLDLTDNQLTTLPLA 440

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
->LtnLeeLdLsqNkIkkiENLde<-
L+ L+ LdL +N+++ + L +
15088 421 LHSLVKLDLTDNQLTTL-PLAG 441

FIG. 11L

LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
-->LtsLqvLdLsnNnLsGeIPsslgn<--
L+sL+ LdL +N+L+ ++P g
15088 421 LHSLVKLDLTDNQLT-TLPL-AGL 442

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
-->LpnLreLdLsnNqLtsLPpgaFqg<--
L++L +LdL +NqLtt+LP ++g
15088 421 LHSLVKLDLTDNQLTTTLPLAGLGG 444

//

FIG.12A

GAP of: FrGcgManager_101_HTAUB3ha_ check: 2817 from: 1 to: 3637

mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_ITA0fLsO_ check: 3059 from: 1 to: 2711

corrected human LGR6 (analysis o - Import - complete

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight:	12	Average Match:	10.000
Length Weight:	4	Average Mismatch:	0.000

Quality:	21826	Length:	3688
Ratio:	8.051	Gaps:	20
Percent Similarity:	84.248	Percent Identity:	84.211

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

FIG. 12B

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLso_

```
901 CCCACAGCTTCGAGGGGCTGCACAAATCTGGAGACACTAGACCTGAACCTAT 950
    |||||
1   ..... GGGCTGCACAAATCTGGAGACACTAGACCTGAATTAT 36

951 AATGAGCTGCAGGAGTTCCCTTGGCTATCCGGACCCTGGGCAGACTGCA 1000
    || |||||
37 AACAAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA 86

1001 AGAATTGGGTTTCCATAAACAAACATCAAGGCTATCCAGAGAAAGCCT 1050
    ||| |||||
87 GGAAGTGGGTTCCATAAACAAACATCAAGGCCATCCAGAAAGGCCT 136

1051 TCATGGGCAACCCCTCTCCTGCAGACAATACATTTTATGACAACCCAATC 1100
    |||||
137 TCATGGGAACCCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186

1101 CAGTTTGTGGGAAGGTCAGCATTCAGTACCTGTCTAAACTGCATACGCT 1150
    |||||
187 CAGTTTGTGGGAAGATCGGCATTCAGTACCTGCCTAAACTCCACACACT 236
```

FIG. 12C

1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCACAGACCTCAAGGCA 1200
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAGGCA 286

1201 CCACTAGCCTGGAGATCCTGACCCCTGACCCCGTGCGGGCATCAGACTGCTC 1250
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
287 CCACCAGCCTGGAGATCCTGACCCCTGACCCCGCGCAGGCATCCGGCTGCTC 336

1251 CCACCGGAGTGTCGCAACAGCTGCCCTAGGCTCCGAATCCTGGAGCTGTC 1300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
337 CCATCGGGATGTGCCAACAGCTGCCCGCAGGCTCCGAGTCTCGGAAGTCTC 386

1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
387 TCACAATCAAATTGAGGAGCTGCCCGCAGCCTGCACAGGTGTCAGAAATTGG 436

1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
437 AGGAAATCGGCCTCCAACACACCGCATCTGGGAAATTGGAGCTGACACC 486

1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536

1451 CCGTGCCATCCACCCTGAGGCTTTCTCAACCCCTTCGATCCTTGGTTAAGC 1500
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
537 CCGGTCCATCCACCCTGAGGCTTCTCCACCCCTGCACTCCCTGGTCAAGC 586

FIG. 12E

1851 CAGTGCAGCCCTGTTCCAGGCCCCCTTCAAGCCCTGCGAGCACCTCTTTGA 1900
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
937 CAGTGTAGCCCTACTCCAGGCCCCCTTCAAGCCCTGTGAGTACCTCTTTGA 986

1901 GAGCTGGGGCATCCGCCCTTGCTGTGTGGGCCATCGTGTCTCCTCGTAC 1950
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
987 AAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTCTCCTCGTGC 1036

1951 TCTGTAAACGGGCTGGTGTCTGTGACAGTCTTTGCCAGCGGACCCAGCCCG 2000
||||| || || ||||| ||||| || || || ||||| || || || |||||
1037 TCTGCAATGGA CTGGTGTCTGTGACCGTGTTCGCTGGCGGGCCTGCCCCC 1086

2001 CTGTCCCCCGTCAAGCTTGTGGTGCGATGGCAGCGGCCAACGCCCT 2050
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1087 CTGCCCCCGGTCAAGTTTGTGTAGGTGCGATTGCAGGCGCCAACACCTT 1136

2051 GACGGGCATTTCCTGTGGTCTCCTGGCCTCTGTGGACGCCCTTGACCTATG 2100
||| ||||| ||||| || || ||||| || || ||||| || || ||||| ||
1137 GACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG 1186

2101 GTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAG 2150
||||| ||||| ||||| ||||| ||||| || || ||||| || || ||||| ||
1187 GTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGCTAGGCTGCCCG 1236

2151 GCTACGGGCTTCCTGGCTGTCCCTGGGTTTCAGAGCGGTCTGGTGTCTGCTGCT 2200
|| || ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
1237 GCCACTGGCTTCCTGGCAGTACTTGGGTCTGGAGGACATCGGTGTCTGCTGCT 1286

FIG. 12F

2201 CACACTGGCGCGGTGCAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCT 2250
||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
1287 CACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCT 1336

2251 ACGGGAAGCGCGGTGCGCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC 2300
| ||||| | || | ||||| || ||||| | || |||||
1337 ATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCCCTAGGCTGC 1386

2301 CTGGCGCTGGCGCGGTGCGCGCAGCACTGCCGCTGGCCTCGGTGGGAGA 2350
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1387 CTGGCACTGGCAGGGCTGGCGCGCGCACTGCCCTGGCCTCAGTGGGAGA 1436

2351 GTATGGCGCCTCCCCACTCTGCCCTGCCCTACGCCCCACCCAGGGCCGGC 2400
|| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1437 ATACGGGCGCCTCCCCACTCTGCCCTGCCCTACGCCCCACCTGAGGGTCAGC 1486

2401 CGGCCGCCCTGGGCTTCGCTGTAGCCCTGGTGATGATGAATCGCTCTGC 2450
| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
1487 CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAATCCTTCTGT 1536

2451 TTCCTGGTGGTGGCGCGCTACATCAAGCTCTACTGTGACCTGCCACG 2500
||||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
1537 TTCCTGGTGGTGGCGCGCTACATCAAACTGTACTGTGACCTGCCCGCG 1586

2501 GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGCCT 2550
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1587 GGGGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGCCT 1636

2551	GGCTCATCTTGCAGATGGCCTCCTCTACTGCCCGTGCCCTTCTCAGC	2600
1637	GGCTCATCTTCGCAGACGGCTCCTCTACTGTCCCGTGCCCTTCTCAGC	1686
2601	TTTGCCCTCCATGCTGGGCTCTTCCCTGTCAACCCGAGGCTGTCAAGTC	2650
1687	TTCGCCCTCCATGCTGGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTC	1736
2651	AGTCCCTTCTGGTGGTGTGCCCTCTGCCCTGCCCTCAACCCACTGCTCT	2700
1737	TGTCCCTGCTGGTGGTGTGCCCTGCCCTGCCCTCAACCCACTGCTGT	1786
2701	ACCTGCTCTTCAACCCCTCACTTCCGGGATGACCTTCGGCGCTCTGGCCA	2750
1787	ACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGCTTCGGCCC	1836
2751	AGCCCTCGGTCCCCAGGGCCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA	2800
1837	CGCGCAGGGACTCAGGGCCCCCTAGCCTATGCTGCGCGCGGAGCTGGA	1886
2801	GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTCTCAGATGTGG	2850
1887	GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG	1936
2851	ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGCTAGAGACC	2900
1937	ATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACC	1986

FIG. 12H

2901 TATGGCTTCCCTTCAGTGACCCCTCATCTCCCGACATCAGCCGGGGCCAC 2950
|||||
1987 TATGGCTTCCCTTCAGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCC 2036
2951 CAGGCTGGAGGGAACCAATTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
|||||
2037 CAGGCTGGAGGCGAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086
3001 ACCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
|||||
2087 ACCCCCAACCTCCATGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136
3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGTGAGCCCTCTGGCCCTCTGG 3100
||
2137 ACGCCAGCAGGTGGAGGCTTGTCTCAGGGGTGGCGCTTTCAGCCCTCTGG 2186
3101 CTCCTCTTTGCTCTCTCACTTGTAATAATCCCT..... 3133
||
2187 CTTGGCCTTTGCTTCAACAGTGTAATAATCCCTCCCATCTCTCTCTCC 2236
3134 .CTCTGTT...TGTC..CTCTCCCATC...CAATGATGGCTGCTTATAA 3174
|||||
2237 CCTCTCTTCCCTTTCCTCTCTCTCCCTCGGTGAATGATGGCTGCTTCTAA 2286
3175 AAGAAAGACAACCTCCAAC.....TCCATAGCAAGATGGCCAAC 3212
||
2287 AACAAATACAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGGCCAG 2336

FIG. 12J

3550 GCTGNGCCAAAGTGCTTCCCTGTAAATAACACTTTGGAAGACATTGAAA 3599
|| :|| || ||||| ||||| ||||| ||||| ||||| |||||
2652 GCCATGCATAAAGACTTCCCTATTAAATAAAGCTTTGGAAGAGATTAAAA 2701

3600 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGGCCGC 3637
|||||||
2702 AAAAAAAAAA..... 2711

FIG. 13A

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nCl_ check: 5092 from: 1 to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102

Matrix made by matblas from blosum62.iiij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248

Quality:	3424	Length:	968
Ratio:	4.646	Gaps:	0
Percent Similarity:	90.773	Percent Identity:	89.281

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nCl_ May 5, 19100 15:04

```
. . .  
201 IPDYAFQNLTSVLVHLHNNRIQHVGTHSEFGLHNLETLDLNYNELQEEP 250  
1 . . . . . GLHNLETLDLNYNKLQEEP 19  
251 LAIRTLGRQLQELGEHNNNIKAIPKAFMGNPILLQTIHFYDNPIQFVGRSA 300  
20 VAIRTLGRQLQELGEHNNNIKAIPKAFMGNPILLQTIHFYDNPIQFVGRSA 69  
301 FQYLSKLHTLSLNGATDIQEFDPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350  
70 FQYLPKLHTLSLNGAMDIEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119  
351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400  
120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169  
401 QALDLSWNAIRAIHPEAFSTLRSVLKLDLTDNQTLTTLPLAGLGGLMHLKL 450  
170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQTLTTLPLAGLGGLMHLKL 219
```


13C

```

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFCKTSGQWQAE 500
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFCKASGQWEAEDL 269
    .
501 HPEEEAPKRPLGLLAGQAEHNYDLDLDELQMGTEDESKPNPSVQCSVPVG 550
    | :||. ||||| ||||| ||||| ||||| : ||||. ||||| |||||
270 HLDDEESSKRPLGLLARQAEHNYDQDLDELQLEMEDSKPHPSVQCSPTPG 319
    .
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAAGPSPLSPVKLV 600
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
320 PFKPCEYLEFESWGIRLAVWAIVLLSVLCNGLVLLTVFAAGGPAPLPVPKFV 369
    .
601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 650
    |||. ||||| ||||| ||||| ||||| : ||||. ||||| ||||| |||||
370 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRAATGFLAV 419
    .
651 LGSEASVLLLTAAVQCSISVTCVRAYGKAPSPGSRAGALGCLALAGLA 700
    ||||| ||||| ||||| : |||. ||||| ||||| ||||| ||||| |||||
420 LGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSRAGVLGCLALAGLA 469
    .
701 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMNNSLCFLVVAGA 750
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNNSFCFLVVAGA 519
    .
751 YIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL 800
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
520 YIKLYCDLPRGDFEAVWDCAMVRHVAVWLIFADGLLYCPVAFLSFASMLGL 569

```

FIG. 13D

[illegible]

FIG. 14A

>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGGTGCAGCCCGCGGACCGGAGCGGAGCTGGGCCACCGCGCGTGCG
TCCGCGCCCGCCAGGTGCCAGTAGCCCGACCGCGAGATGCCAGCCCGCGGG
GCTCCGGCGCTATGGCTTTGCGCCGCGTGTGCGCTTCCGGAGGCGCGCGCCC
CCAGCCCGCCCGGCCACCGCTGCCCGCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGTCTGAGCTCGGCTGTCCGCCGTTCCGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGCCCTTT
CCACCACCTGGCTTCTTGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTGTCTCTACAGCCCTGAATACTGTGATGCTGCAGAAACAATCAGCT
GGAGGAAATCCCGCAGAGGCGCTGTGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCTCTCCCTCCGCCA
CCTCTGGCTGGACGACAATGCACCTCACGGAGATCCCTGTCAAGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCCTGGCCCTCAACCGCATCAGCCACATCCCAGACTACGCGTT
CCAGAATCTCACAGCCCTTGTGTGCTGCTGCAATTGCAATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCTGTGGCCATCCGGACCCCTGGGCAGACTGCAGGAACCTGGGTCCATAA
CAACAACATCAAGGCCATCCAGAAAGGCCCTTCAATGGGAACCTCTGCTACAGACGAT
ACACTTTTATGATAACCAATCCAGTTTGTGGGAAGATCGGCATTCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCAACAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCATCGGG
GATGTGCCAACAGCTGCCAGGCTCCGAGTCCCTGGAACTGTCTCACAATCAAATTGAGGA
GCTGCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAATCGGCTCCCAACAACCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCTGAGGCCCTTCTCCACCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACCAAGCTGACCACTGCCCTGGCTGGACTTGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCC

FIG. 14B

AAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCAGTGCTGTCCCTATGGGATGTGTGC
CAGCTTCTCAAGGCTCTGGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAGGCCCTGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAAGCCACACCCAGTGTCAGTGTAG
CCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCT
GGCCGTGTGGCCATCGTGTCTCCGTCTCCGTCTGCAATGGA¹CTGGTGTGCTGACCCGT
GTTCCGTGGCGGCTGCCCTGCCCTCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAAACACCTTGACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTGTAGTACGGAGCCCGCTGGGAGACGGGCTAGGCTGCCGGCCACTGG
CTTCCCTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTCACTCTGGCCGCGAGTGCA
GTGCAGCGTCTCCGTCTCCGTGTCCGGCCTATGGGAAGTCCCTCCCTGCGCAGCGT
TCGAGCAGGGTCCTAGGCTGCCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGC
CTCAGTGGGAGAAATACGGGGCTCCCACTCTGCCCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAAC²TCTTCTGTTCTCTGGT
CGTGGCCGGTGCCATCAAACTGTACTGTGACCTGCCGGGCGGCACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTA
CTGTCCCGTGGCCTTCCCTCAGCTTCGCCCTCCATGCTGGCCTCTTCCCTGTCAAGCCCGA
GGCCGTCAAGTCTGTCCCTGTGGTGTGCTGCCCTGCCCTGCCCTCAACCCACTGCT
GTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGGGCTTCGGCCCGCGCAGG
GGACTCAGGGCCCTAGCCCTATGCTGCGGCGGGAGCTGGAGAAGAGCTCCTGTGATTC
TACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGG
GCGGCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCTCATCTCCTGTTCAGCA
GCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCAACCCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCCCTCTGGCTTGCCCTTTGCTTCACA
CGTGTAATAATCCCTCCCACTTCTTCTTCCCTCTCTTCCCTTCTCTCTCTCTCTCTCTC
GGTGAATGATGGCTGCTTCTAAACAAATACAAACCAAACTCAGCAGTGATCTATAGC

FIG. 14C

AGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCTCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTTCCCTTGGCCCTTCCTCAGCTTACCTTGATACCTGGCCCTCTTC
CTTGTCATGCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTTAAGGGAATGA
GGGAAGTAAAGACAGTGAAGGGTGGAGGGTTGATCAGGGCACAGTGACAGGGAGACCT
CACARAAAAGGCCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCCATGCATAAARACTTCCTATTAAAAATAAGCT
TTGGRAGAGATT

FIG. 15

>15088

MPSPGLRALWLCASRRAGGAPQPGPTACPApchQEDGIMLSADcSELGLSAVPGDLDP LTAYLDLSMNNLT
ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKIIMLQNNQLGGIPAEALWELPSLSQLRDLNLI SLVPERSE
EGLSSLRHLWLDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSVLHLHNNRIQH LGTHSFEGLHNLE
TLDLNYNKLQEEFVAIRTLGRLLQELGFHNNNIKAIPKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAM
DIQFFPDLKGTTSLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEI GLQHNR IWEIGADTFS
QLSSLQALDLSWNAIRS IHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQA FSKDSFPKLRILEVP
YAYQCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSP TPGPFK
PCEYLFESWGIRLAVWAI VLLSVLCNGLVLLTVFAGGPAPLPVPKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEY
GARWETGLGCRATGFLAVLGSEASVLLTLAAVQCSVSVSCVRAYGKSPSLG SVRAGVLGCLALAGLAAALPLASVGEY
GASPLCLPYAPPEGQPAALGFTVALVMN SFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLI FADGLLYCPVA
FLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLENPHFRDDLRRLLRPRAGDSG PLAYAAAGELEKSSCDSTQA
LVAFSDVDLILEASEAGRPPGLETYGFPSVTLISCCQQPGAPRLEGSHC VEPEGNHFGNPQPSMDGELL LRAEGSTPAGG
GLSGGGGFQPSGLAFASHV*

FIG. 16A

protein alignment between mouse and human
> LGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102

Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248
Quality:	4495	Length:	968
Ratio:	4.653	Gaps:	2
Percent Similarity:	91.097	Percent Identity:	89.855

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

FrGcgManager_9_PBA0KgkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

FIG. 16B

	Mouse	Human
1	MHSPFGLLALWLCASARGGSDPQPGGRPACPAPCHCQEDGIMLSA	50
1	MPSPFGLRALWLCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA	50
51	DCSELGLSVVPADLDPLTAYLDLSMNNLTQLPGLFHHLRFELELRLSGN	100
51	DCSELGLSAVPGDLDPLTAYLDLSMNNLTQLPGLFHHLRFELELRLSGN	100
101	HLSHIPGQAFSGLSKILMLQSNQLRGIPAEALWELPSLQSLRLDANLI	150
101	HLSHIPGQAFSGLSKILMLQNNQLGGIPAEALWELPSLQSLRLDANLI	150
151	SLVPERSEGLSSLRHLWLDNALT EIPVRALNNLPALQAMTLALNHIRH	200
151	SLVPERSEGLSSLRHLWLDNALT EIPVRALNNLPALQAMTLALNRISH	200
201	IPDYAFQNLTSLVVHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEEP	250
201	IPDYAFQNLTSLVVHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEEP	250
251	LAIRTLGRLQELGEHNNNIKA IPEKAFMGNPLLQTIHFYDNPIQFVGRSA	300
251	VAIRTLGRLQELGEHNNNIKA IPEKAFMGNPLLQTIHFYDNPIQFVGRSA	300
301	FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ	350
301	FQYLPKLHTLSLNGAMD IQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ	350

FIG. 16C

```

351 LPRLRILELSHNQIEELPSLHRCQKLEI GLRHNRIKEIGADTFSQLGSL 400
    ||||:|||||||||||||||||.||||| ||||| ||||| ||
351 LPRLRVLELSHNQIEELPSLHRCQKLEI GLQHNRIWEIGADTFSQLSSL 400

401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
    ||||| |||||.||||| ||||| ||||| ||||| ||||| |||||
401 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSQWQAEDE 500
    ||||| ||||| ||||| ||||| ||||| |||.||||| |||||:||||
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFKAQSGQWEAEDL 500

501 HPEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
    | :|||.||||| ||||| |||||: |||||.||||| ||||| ||
501 HLDDEESSKRPLGLLARQAENHYDQDLDLDELQLEMEDSKPHPSVQCSPTPG 550

551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV 598
    |||||:||||| ||||| ||||| ||||| ||||| |||.||| |||
551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 600

599 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 648
    |||.||||| ||||| ||||| |||||:||||.||||| ||||| |||||
601 VGAAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRAATGFLAV 650

649 LGSEASVLLLTIAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 698
    ||||| ||||| |||||:|||.||||| ||||| ||||| ||||| |||||
651 LGSEASVLLLTIAAVQCSVSVCVRAYGKSPSLGSVRAGVLGCLALAGLA 700

```

